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#2

RAW SEQUENCE LISTING

DATE: 10/18/2001 TIME: 09:43:56

PATENT APPLICATION: US/09/964,412

Input Set : A:\ES.txt

SEQUENCE LISTING

Output Set: N:\CRF3\10182001\I964412.raw

ENTERED

```
(1) GENERAL INFORMATION:
      6
             (i) APPLICANT: de la Monte, Suzanne
      7
                             Wands, Jack R.
      9
            (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
                                      Screening Drugs Effective for the Treatment or Prevention
     10
                                      of Alzheimer's Disease
     11
     13
           (iii) NUMBER OF SEQUENCES: 14
            (iv) CORRESPONDENCE ADDRESS:
     15
     16
                   (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
     17
                   (B) STREET: 1100 New York Ave., Suite 600
     18
                  (C) CITY: Washington
                  (D) STATE: DC
     19
     20
                   (E) COUNTRY: USA
     21
                  (F) ZIP: 20005-3934
     23
             (V) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
     25
                  (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/964,412
C--> 30
C-->31
                  (B) FILING DATE: 28-Sep-2001.
     32
                  (C) CLASSIFICATION:
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                   (A) NAME: Esmond, Robert W.
                  (B) REGISTRATION NUMBER: 32,893
     36
     37
                  (C) REFERENCE/DOCKET NUMBER: 0609.4370000
     39
            (ix) TELECOMMUNICATION INFORMATION:
     40
                  (A) TELEPHONE: 202-371-2600
     41
                  (B) TELEFAX: 202-371-2540
        (2) INFORMATION FOR SEQ ID NO: 1:
     44
             (i) SEQUENCE CHARACTERISTICS:
     46
     47
                  (A) LENGTH: 1442 base pairs
                  (B) TYPE: nucleic acid
     48
                  (C) STRANDEDNESS: double
     49
     50
                  (D) TOPOLOGY: both
     52
            (ii) MOLECULE TYPE: cDNA
     55
            (ix) FEATURE:
     56
                  (A) NAME/KEY: CDS
     57
                  (B) LOCATION: 15..1139
     61
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     63 TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
                                                                                  50
     64
                         Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
     65
                           1
                                                               10
     67 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC
                                                                                  98
     68 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
```





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69 15	20	25	
71 GAT TCT CCT GCC TCA			ATG TGC 146
72 Asp Ser Pro Ala Ser			
73 30	35	40	
75 ACC CAC GCT CGG CTA		TTT TTA GTA GAG ATG	GAG TTT 194
76 Thr His Ala Arg Leu			
77 45	50	55	60
79 CTC CAT GTT GGT CAG	GCT GGT CTC GAA	CTC CCG ACC TCA GAT	GAT CCC 242
80 Leu His Val Gly Gln			
81 65		70	75
83 TCC GTC TCG GCC TCC	CAA AGT GCT AGA	TAC AGG ACT GGC CAC	CAT GCC 290
84 Ser Val Ser Ala Ser	Gln Ser Ala Arg	Tyr Arg Thr Gly His	His Ala
85 80	85	90	
87 CGG CTC TGC CTG GCT	AAT TTT TGT GGT	AGA AAC AGG GTT TCA	CTG ATG 338
88 Arg Leu Cys Leu Ala	Asn Phe Cys Gly	Arg Asn Arg Val Ser	Leu Met
89 95	100	105	
91 TGC CCA AGC TGG TCT	CCT GAG CTC AAG	CAG TCC ACC TGC CTC	AGC CTC 386
92 Cys Pro Ser Trp Ser	Pro Glu Leu Lys	Gln Ser Thr Cys Leu	Ser Leu
93 110	115	120	
95 CCA AAG TGC TGG GAT			
96 Pro Lys Cys Trp Asp			
97 125	130	135	140
99 TTA TTT TTT TTA AGA			
100 Leu Phe Phe Leu Ar			
101 14		150	155
103 CAG TGG TGT GAT CA			
104 Gln Trp Cys Asp Hi			
105 160	16		
107 CAT CCT CCT GCC TC 108 His Pro Pro Ala Se			
106 HIS PIO PIO ATA SE 109 175	180	185	Met III5
111 CAC TAC ACC TGG CT			G AGA CAG 626
112 His Tyr Thr Trp Le			
112 HIS 191 IIII 11P De	195	200	
115 AGT CTC AAC TCT GT			CTT GGC 674
116 Ser Leu Asn Ser Va			
119 205	210	215	220
121 TCA CTG CAA CCT CT			C CCC AGC 722
122 Ser Leu Gln Pro Le			
123 22		230	235
125 CTC CTG AGT AGC TG	G GAC TAC AGG CG	C CCA CCA CGC CTA GC	T AAT TTT 770
126 Leu Leu Ser Ser Tr			
		5 250	
129 TTT GTA TTT TTA GT	TA GAG ATG GGG TT	C ACC ATG TTC GCC AGO	G TTG ATC 818
130 Phe Val Phe Leu Va			
131 255	260	265	
133 TTG ATC TCT GGA CC	CT TGT GAT CTG CC	T GCC TCG GCC TCC CA	A AGT GCT 866
134 Leu Ile Ser Gly Pr			
135 270	275	280	



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															TTT Phe		914
	285			1		290				3	295					300	
															CAA		962
142 143	Leu	Phe	Glu	Met	Glu 305	Ser	His	Ser	Val	Thr 310	Gln	Ala	Gly	Val	Gln 315	Trp	
145	CCA	AAT	CTC	GGC	TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	CTC	AAG	CGA	TTC	1010
146	Pro	Asn	Leu	Gly	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	
147				320					325					330			
149	TCC	TGT	CTC	AGC	CTC	CCA	AGC	AGC	TGG	GAT	TAC	GGG	CAC	CTG	CCA	CCA	1058
	Ser	Cys		Ser	Leu	Pro	Ser		\mathtt{Trp}	Asp	Tyr	Gly	His	Leu	Pro	Pro	
151			335					340					345				
															CCA		1106
			Ala	Asn	Phe	Cys		Phe	Ile	Arg	GLy	_	Val	Ser	Pro	Tyr	
155		350	000	maa	mam	CA A	355	ООШ	C 2 C	СШС	7.00	360	7007	7.Cm /	aaama	23 C C C C C	1150
												TGAC	CCA	CCT (GCCT	CAGCCT	1159
	Leu 365	ser	СТА	Trp	ser		THE	Pro	Asp	ьeu	_						
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																TGGCTT	
																GTTACA	1339
																ICAGTA	
	GTA															ICAGIA	1442
172								NO: 2			mon	CCA					1442
174	•																
174 (i) SEQUENCE CHARACTERISTICS: 175 (A) LENGTH: 375 amino acids																	
T / D			(]	A) LI	ENGTI					ds							
178			•	•			75 ar	nino		ls							
			(I	3) TY	PE:	H: 37	75 ar no ac	mino cid		ls							
178		(ii	(I	3) TY O) T(PE:	H: 37 amin DGY:	75 ar no ac line	mino cid ear		ds		-					
178 179		•	I) I) IOM (B) TY D) T(LECUI	(PE: OPOLO LE TY	H: 37 amin DGY: YPE:	75 an no ao line prot	mino cid ear	acio		D: 2:	:					
178 179 181 183		(xi	(I (I) MOI) SE(3) TY C) TO LECUI QUENO	PE: OPOLO LE TY CE DI	H: 37 amin DGY: YPE: ESCRI	75 ar no ac line prot	mino cid ear tein ON: S	acio	ED NO			Asn	Gly	Ala	Ile	
178 179 181 183 185 186	Met 1	(xi Glu	(I (I) MOI) SE(Phe	3) TY D) TO LECUI QUENO Ser	PE: POLC LE TY CE DI Leu 5	amin OGY: YPE: ESCRI	75 and according to the second	mino cid ear tein ON: S	acio SEQ I	ID NO Leu 10	Glu	Cys		-	15		
178 179 181 183 185 186 188	Met 1	(xi Glu	(I (I) MOI) SE(Phe	3) TY D) TO LECUI QUENO Ser Arg	PE: POLC LE TY CE DI Leu 5	amin OGY: YPE: ESCRI	75 and according to the second	mino cid ear tein ON: S	EEQ 3 Arg	ID NO Leu 10	Glu	Cys		-			
178 179 181 183 185 186 188	Met 1 Ser	(xi Glu Ala	(H (I) MOI) SE(Phe His	3) TY D) TO LECUI QUENO Ser Arg 20	PE: POLO LE TY CE DI Leu 5 Asn	amin OGY: YPE: ESCRI Leu	75 and a control of the control of t	mino cid ear tein ON: S Pro	EEQ 3 Arg Pro	ID NO Leu 10 Gly	Glu Ser	Cys Ser	Asp	Ser 30	15 Pro	Ala	
178 179 181 183 185 186 188 189	Met 1 Ser	(xi Glu Ala	(H (I) MOI) SE(Phe His	3) TY D) TO LECUI QUENO Ser Arg 20	PE: POLO LE TY CE DI Leu 5 Asn	amin OGY: YPE: ESCRI Leu	75 and a control of the control of t	mino cid ear tein ON: S Pro Leu	EEQ 3 Arg Pro	ID NO Leu 10 Gly	Glu Ser	Cys Ser	Asp Thr	Ser 30	15 Pro		
178 179 181 183 185 186 188 189 191	Met 1 Ser	(xi Glu Ala Ala	(H (I) MOI) SE(Phe His Ser 35	3) TY D) TO LECUI QUENC Ser Arg 20 Pro	PE: POLO LE TY LE DI Leu 5 Asn Val	amin DGY: YPE: ESCRI Leu Leu	75 and a control of the control of t	mino cid ear tein ON: S Pro Leu Ile 40	EEQ Arg Pro 25	Leu 10 Gly	Glu Ser Met	Cys Ser Cys	Asp Thr 45	Ser 30 His	15 Pro Ala	Ala Arg	
178 179 181 183 185 186 188 189 191 192 194	Met 1 Ser	(xi Glu Ala Ala Ile	(H (I) MOI) SE(Phe His Ser 35	3) TY D) TO LECUI QUENC Ser Arg 20 Pro	PE: POLO LE TY LE DI Leu 5 Asn Val	amin DGY: YPE: ESCRI Leu Leu	75 and 15	mino cid ear tein ON: S Pro Leu Ile 40	EEQ Arg Pro 25	Leu 10 Gly	Glu Ser Met	Cys Ser Cys Phe	Asp Thr 45	Ser 30 His	15 Pro	Ala Arg	
178 179 181 183 185 186 188 189 191 192 194 195	Met 1 Ser Ser	(xi Glu Ala Ala Ile 50	(H (I) MOI) SE(Phe His Ser 35 Leu	3) TY D) TO DECUI QUENC Ser Arg 20 Pro	PE: POLC LE TY LE DI Leu 5 Asn Val	aminogy: YPE: YPE: Leu Leu Ala	75 and 15	nino cid ear tein ON: S Pro Leu Ile 40 Val	EEQ Arg Pro 25 Thr	Leu 10 Gly Gly Met	Glu Ser Met Glu	Cys Ser Cys Phe 60	Asp Thr 45 Leu	Ser 30 His	15 Pro Ala Val	Ala Arg Gly	
178 179 181 183 185 186 188 191 192 194 195 197	Met 1 Ser Ser Leu	(xi Glu Ala Ala Ile 50	(H (I) MOI) SE(Phe His Ser 35 Leu	3) TY D) TO DECUI QUENC Ser Arg 20 Pro	PE: POLC LE TY LE DI Leu 5 Asn Val	aminogy: YPE: YPE: Leu Ala Phe Leu	75 and 15	nino cid ear tein ON: S Pro Leu Ile 40 Val	EEQ Arg Pro 25 Thr	Leu 10 Gly Gly Met	Glu Ser Met Glu Asp	Cys Ser Cys Phe 60	Asp Thr 45 Leu	Ser 30 His	15 Pro Ala	Ala Arg Gly Ala	
178 179 181 183 185 186 188 191 192 194 195 197 198	Met 1 ser Ser Leu Gln 65	(xi Glu Ala Ala Ile 50 Ala	(H (I) MOI) SE(Phe His Ser 35 Leu	Arg Pro Tyr Leu	PE: POLC LE TY LE DI Leu 5 Asn Val Phe Glu	aminogy: YPE: YPE: Leu Leu Ala Phe Leu 70	75 and a control of the control of t	nino cid ear tein ON: S Pro Leu Ile 40 Val	EEQ Arg Pro 25 Thr Glu	Leu 10 Gly Gly Met	Glu Ser Met Glu Asp 75	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Val	15 Pro Ala Val Ser	Ala Arg Gly Ala 80	
178 179 181 183 185 186 188 191 192 194 195 197 198 200	Met 1 ser Ser Leu Gln 65	(xi Glu Ala Ala Ile 50 Ala	(H (I) MOI) SE(Phe His Ser 35 Leu	Arg Pro Tyr Leu	PE: POLO LE TY LE DI Leu 5 Asn Val Phe Glu Arg	aminogy: YPE: YPE: Leu Leu Ala Phe Leu 70	75 and a control of the control of t	nino cid ear tein ON: S Pro Leu Ile 40 Val	EEQ Arg Pro 25 Thr Glu	ID NO Leu 10 Gly Gly Met Asp	Glu Ser Met Glu Asp 75	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Val	15 Pro Ala Val Ser Cys	Ala Arg Gly Ala 80	
178 179 181 183 185 186 188 191 192 194 195 197 198 200 201	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln	(H (I) MOI) SE(Phe His Ser 35 Leu Gly	Arg Pro Tyr Leu Ala	PE: POLO LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr	75 and a control of the control of t	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr	EEQ Arg Pro 25 Thr Glu Ser	ID NO Leu 10 Gly Gly Met Asp His 90	Glu Ser Met Glu Asp 75 His	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Val Leu	15 Pro Ala Val Ser Cys 95	Ala Arg Gly Ala 80 Leu	
178 179 181 183 185 186 188 191 192 194 195 197 198 200 201	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln	(H (I) MOI) SE(Phe His Ser 35 Leu Gly	Arg Pro Tyr Leu Ala	PE: POLO LE TY LE DI Leu 5 Asn Val Phe Glu Arg 85	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr	75 and a control of the control of t	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr	EEQ Arg Pro 25 Thr Glu Ser	ID NO Leu 10 Gly Gly Met Asp His 90	Glu Ser Met Glu Asp 75 His	Cys Ser Cys Phe 60 Pro	Asp Thr 45 Leu Ser	Ser 30 His Wal Leu	15 Pro Ala Val Ser Cys	Ala Arg Gly Ala 80 Leu	
178 179 181 183 185 186 188 191 192 194 195 197 198 200 201 203 204	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln Asn	(H (II) MOI) SE() Phe His Ser 35 Leu Gly Ser Phe	Arg Pro Tyr Leu Ala Cys 100	PE: OPOLO LE TY CE DI Leu 5 Asn Val Phe Glu Arg 85 Gly	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr Arg	75 and 10	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr	EQ Arg Pro 25 Thr Glu Ser Gly Val 105	ID NO Leu 10 Gly Gly Met Asp His 90 Ser	Glu Ser Met Glu Asp 75 His	Cys Ser Cys Phe 60 Pro Ala Met	Asp Thr 45 Leu Ser Arg	Ser 30 His Wal Leu Pro 110	15 Pro Ala Val Ser Cys 95	Ala Arg Gly Ala 80 Leu Trp	
178 179 181 183 185 186 188 191 192 194 195 197 198 200 201 203 204	Met 1 Ser Ser Leu Gln 65 Ser	(xi Glu Ala Ala Ile 50 Ala Gln Asn	(H (II) MOI) SE() Phe His Ser 35 Leu Gly Ser Phe	Arg Pro Tyr Leu Ala Cys 100	PE: OPOLO LE TY CE DI Leu 5 Asn Val Phe Glu Arg 85 Gly	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr Arg	75 and 10	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr	EQ Arg Pro 25 Thr Glu Ser Gly Val 105	ID NO Leu 10 Gly Gly Met Asp His 90 Ser	Glu Ser Met Glu Asp 75 His	Cys Ser Cys Phe 60 Pro Ala Met	Asp Thr 45 Leu Ser Arg	Ser 30 His Wal Leu Pro 110	15 Pro Ala Val Ser Cys 95 Ser	Ala Arg Gly Ala 80 Leu Trp	
178 179 181 183 185 186 189 191 192 194 195 197 198 200 201 203 204 206 207	Met 1 Ser Leu Gln 65 Ser Ala	(xi Glu Ala Ala Ile 50 Ala Gln Asn Pro	(H (II) MOI) SE(I) Phe His Ser 35 Leu Gly Ser Phe Glu 115	D) TO D) TO D) TO D) TO DUENO Ser Arg 20 Pro Tyr Leu Ala Cys 100 Leu	PE: OPOLO LE TY Leu S Asn Val Phe Glu Arg 85 Gly Lys	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr Arg	75 and 10	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr Arg Thr 120	EQ Arg Pro 25 Thr Glu Ser Gly Val 105 Cys	ID NO Leu 10 Gly Gly Met Asp His 90 Ser Leu	Glu Ser Met Glu Asp 75 His Leu	Cys Ser Cys Phe 60 Pro Ala Met Leu	Asp Thr 45 Leu Ser Arg Cys Pro 125	Ser 30 His Wal Leu Pro 110 Lys	15 Pro Ala Val Ser Cys 95 Ser	Ala Arg Gly Ala 80 Leu Trp	
178 179 181 183 185 186 189 191 192 194 195 197 198 200 201 203 204 206 207	Met 1 Ser Leu Gln 65 Ser Ala	(xi Glu Ala Ala Ile 50 Ala Gln Asn Pro	(H (II) MOI) SE(I) Phe His Ser 35 Leu Gly Ser Phe Glu 115	D) TO D) TO D) TO D) TO DUENO Ser Arg 20 Pro Tyr Leu Ala Cys 100 Leu	PE: OPOLO LE TY Leu S Asn Val Phe Glu Arg 85 Gly Lys	aminogy: YPE: YPE: Leu Ala Phe Leu 70 Tyr Arg	75 and 10	nino cid ear tein ON: S Pro Leu Ile 40 Val Thr Thr Arg Thr 120	EQ Arg Pro 25 Thr Glu Ser Gly Val 105 Cys	ID NO Leu 10 Gly Gly Met Asp His 90 Ser Leu	Glu Ser Met Glu Asp 75 His Leu	Cys Ser Cys Phe 60 Pro Ala Met Leu	Asp Thr 45 Leu Ser Arg Cys Pro 125	Ser 30 His Wal Leu Pro 110 Lys	15 Pro Ala Val Ser Cys 95 Ser Cys	Ala Arg Gly Ala 80 Leu Trp	



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Input Set : A:\ES.txt

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213	145					150					155					160	
215	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala	
216					165				-	170					175		
218	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp	
219				180			_		185	-				190		~	
	Leu	Tle	Phe		Phe	Tle	Phe	Asn			Arα	Gln	Ser		Δsn	Ser	
222.			195	110	2 110	110	1 110	200	1110	LCu	1119	O = 11	205	LCu	21011		
		Πh ~		א ד ה	C1.	1701	C15		7 ~~~))	T 0	C1		Т о	<i>c</i> 15	Dwo	
	Val		GIII	мта	СТУ	val		пр	Arg	ASII	ьeu	-	ser	ьец	GIII	PIO	
225		210	_		_1	_	215	_,		_	_	220	_		_	_	
	Leu	Pro	Pro	GTA	Phe		Leu	Phe	Ser	Cys		Ser	Leu	Leu	Ser		
228	225					230					235					240	
230	\mathtt{Trp}	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu	
231					245					250					255		
233	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arq	Leu	Ile	Leu	Ile	Ser	Gly	
234				260					265	,				270		•	
	Pro	Cvs	Asn		Pro	Δla	Ser	Δla		Gln	Ser	Δla	Glv		Thr	Glv	
238		Cys	275	LCu	110	AIu	Jei		261	GIII	Der	AIG		116	1 111.	GIY	
		0		TT/	3 J =	3	T	280	Dl	3	Dl	G	285	D1	a 1	W = 4	
	Val		HIS	His	Ala	Arg		тте	Pne	Asn	Pne	_	Leu	Pne	GIu	met	
241	_	290	_				295					300					
243	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	\mathtt{Trp}	Pro	Asn	Leu	Gly	
244	305					310					315					320	
246	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser	
247					325			_		330				_	335		
249	Leu	Pro	Ser	Ser	Trp	Asp	Tvr	Glv	His	Leu	Pro	Pro	His	Pro	Ala	Asn	
250				340			-1-		345				11_0	350			
	Phe	Cvc	Tlo		T10	λνα	C137	C137		Cor	Dro	Птт	T 011		C1 11	m~~	
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253	0	01	355	D	•	T	3	360					365				
	Ser		THE	Pro	Asp	Leu											
256	_	370					375		_								
	(2)	INFO	DRMAI	rion	FOR	SEQ	ID N	10: 3	3:								
260		(i)	SEC	QUENC	CE CI	IARAC	CTERI	STIC	CS:								
261			(P	A) LE	ENGT	H: 13	881 k	oase	pair	îs.							
262			(E	3) TY	PE:	nucl	leic	acid	i								
263			((C) S7	RANI	DEDNE	ESS:	douk	ole	-		-					
264			(1) TO	POL	OGY:	both	ı						•		•	
266		(ii)	•	ÉCUI													
271		•		QUENC					SEO 1	רם אכ	١٠ ٦٠						
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																CTCCCC	120
																TAGTA	180
279	GAGA	TGGA	GT I	TAAC	CTCCF	AT GI	TGGI	CAGG	CTO	GTCI	CGA	ACTO	CCCGA	ACC 1	CAGA	TGATC	240
281	TCCC	GTCI	CG G	SCCT	CCC	AA AC	TGCI	GAGA	TTA	CAGG	CAT	GAGC	CCACC	CAT	SCCCG	GCCTC	. 300
283	TGCC	TGGC	TA A	LTTTI	TGT	GG TA	GAAA	CAGO	GTI	TCAC	CTGA	TGTT	GCCC	CAA G	CTG	TCTCC	360
285	TGAG	CTCA	AG C	CAGTO	CAC	CT GC	CTCA	GCCI	CCC	CAAAC	TGC	TGGG	SATTA	CA C	GCGT	CAGCC	420
287																CAGGAT	480
289																CAATCC	540
291																TAATT	600
293												_	-			SAGTGC	660
230	AG10	1000C	AA 1	CIT	GCTC	A CI	.GCAA		. 160		<i>.</i> ८७७	GITC	MAGI	.IA I	TCTC	CTGCC	720



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PATENT APPLICATION: US/09/964,412

298	CCAGCCTCCT GAGTAGCTGG	GACTACAGGC	GCCCACCACG	CCTAGCTAAT	TTTTTTGTAT	780
300	TTTTAGTAGA GATGGGGTTT	CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
302	GATCTGCCTG CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
304	CTATTTTAA TTTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
306	AATGGCAAAT CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
308	AGCCTCCCAA GCAGCTGGGA	TTACGGGACC	TGCACCACAC	CCCGCTAATT	TTTGTATTTT	1080
310	CATTAGAGGC GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
312	CCCACCTGCC TCAGCCTTCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
314	GGCTAATTTG GAATAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
316	TCAAACTTCT GGCTTCAGTC	AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
318	TTTTAAACAG TTACATCTTT	ATTTTAGTAT	ACTAGAAAGT	AATACAATAA	ACATGTCAAA	. 1380
320	C					1381
322	(2) INFORMATION FOR SE	EQ ID NO: 4:	•			
324	(i) SEQUENCE CHAR	RACTERISTICS	S:			
325	(A) LENGTH:	1418 base p	pairs			
326	(B) TYPE: nu	cleic acid			-	
327	(C) STRANDEL	NESS: both				
328	(D) TOPOLOGY	: both				
330	(ii) MOLECULE TYPE	E: cDNA				
335	(xi) SEQUENCE DESC	CRIPTION: SE	EQ ID NO: 4:	•		
337	TTTTTTTTT GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
339	CTCAGCTCAC CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
341	AGTAGGCTGG GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGTATT	TTTTTTTAGT	180
343	AGAGATGGAG TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
345	CCCGTCTCGG CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
347	GGCTAATTTT TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
349	CAAGCAGTCC ACCTGCCTCA	GCCTCCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
351	TGGCCTTTTT ATTTTATTTT	TTTTAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
355	GCAGTGGTGT GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
357	TCAGCCTCCC AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTTAT	600
359	TTTTATTTTT AATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
361	GCGCAATCTT GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAGTTATTCT	CCTGCCCCAG	720
363	CCTCCTGAGT AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATTTTT	TTGTATTTTT	780
365	AGTAGAGATG GGGTTTCACC	ATGTTCGCCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
367	CTGCCTGCCT CGGCCTCCCA	AAGTGCTGGG	ATTACAGGAC	GTGACGCCCA	CCGCCCGGCC	900
369	TATTTTAAT TTTTGTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
371	ATGGCCAAAT CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
373	CAGCCTCCCA AGCAGCTGGG	ATTACGGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTTGTATT	1080
375	TTCATTAGAG GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACTCC	TGACCTCAGG	1140
377	TGACCCACCT GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCCAGC	1200
379	CGGCTAATTT AGATAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
381	GTCTCAAACT TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
383	ATTTTTAAAC AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
385	AACCTGCAAA TTCGAGTAGT	ACAGAGTCTT	TTATAACT			1418
387	(2) INFORMATION FOR SE	EQ ID NO: 5:				
389	(i) SEQUENCE CHAR	RACTERISTICS	S:			
390	(A) LENGTH:	22 base pai	rs			
391	(B) TYPE: nu	cleic acid				
392	(C) STRANDED	NESS: singl	_e	•		

VERIFICATION SUMMARY

DATE: 10/18/2001

PATENT APPLICATION: US/09/964,412

TIME: 09:43:57

Input Set : A:\ES.txt

Output Set: N:\CRF3\10182001\I964412.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]